

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 4, 2003, 12:27:54 ; Search time 732 Seconds

(without alignments)
4844.670 Million cell updates/sec

Title: US-10-082-894-1

Perfect score: 1719

Sequence: 1 gtttaattaccgaatttga.....aaatctcgtataaaaatt 1719

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
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- 15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	261.4	15.2	6048	8	US-08-781-986A-128
2	222.2	12.9	1620	10	US-09-895-913A-105
3	175.6	10.2	1041	10	US-09-974-300-696
4	161.2	9.4	881	10	US-09-974-300-5220
5	84	4.9	1728	10	US-09-938-842A-2675
C 6	81.4	4.7	484	9	US-09-159-469-34
C 7	81.4	4.7	484	9	US-09-798-042-34
8	69.4	4.0	400	8	US-08-781-986A-782
C 9	51.8	3.0	264	10	US-09-974-300-894
10	42.6	2.5	279	9	US-09-294-093B-4299
C 11	42.4	2.5	2000	10	US-09-938-842A-2831
C 12	40	2.3	640681	10	US-09-790-988-1
13	39.8	2.3	2861	9	US-09-887-586A-55
14	39.8	2.3	2861	9	US-09-903-012-55
15	39.8	2.3	2861	11	US-09-900-797-55
16	39.8	2.3	2861	13	US-10-041-007-3

17	39.4	2.3	1407	9	US-09-815-242-8836
18	39.4	2.3	7953	8	US-08-781-986A-152
C 19	38.8	2.3	19553	10	US-09-764-847-1425
C 20	38.8	2.3	19553	14	US-10-092-154-1425
C 21	38.6	2.2	2000	10	US-09-933-842A-4130
22	38.6	2.2	640681	10	US-09-790-988-1
23	38.4	2.2	350	9	US-09-864-761-23424
24	38.4	2.2	600	9	US-09-864-761-6690
C 25	37.8	2.2	507	13	US-10-027-632-200181
26	37.8	2.2	521	14	US-10-255-536-138
27	37.8	2.2	1404	9	US-09-815-242-4475
28	37.8	2.2	1407	9	US-09-815-242-8257
C 29	37.8	2.2	6298	14	US-10-239-676-63
C 30	37.8	2.2	6665	14	US-10-239-676-4
C 31	37.6	2.2	420	10	US-09-764-877-2144
32	37.6	2.2	1344	10	US-09-887-576-519
33	37.6	2.2	1344	10	US-09-887-576-543
34	37.6	2.2	2000	10	US-09-938-842A-5075
35	37.6	2.2	2002	10	US-09-887-576-28
36	37.4	2.2	651	11	US-09-791-932-42
C 37	37.4	2.2	1164	13	US-10-027-632-31828
C 38	37.2	2.2	2266	11	US-09-978-418-11
39	37.2	2.2	3625	10	US-09-070-927A-42
C 40	37	2.2	2000	10	US-09-938-842A-4050
41	37	2.2	2000	10	US-09-938-842A-4173
42	37	2.2	20261	9	US-09-764-878-325
43	37	2.2	20261	14	US-10-079-854-325
C 44	37	2.2	32768	10	US-09-070-927A-128
45	36.8	2.1	1959	9	US-09-864-761-4012

ALIGNMENTS

RESULT 1

US-08-781-986A-128
; Sequence 128, Application US/08781986A
; Publication No. US20030054436A1

GENERAL INFORMATION:
APPLICANT: Charles Kunsch

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/781.986A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Bob

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 309-8504

TELEFAX: (301) 309-8512

INFORMATION FOR SEQ ID NO: 128:

SEQUENCE CHARACTERISTICS:

LENGTH: 6048 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear
US-08-781-986A-128

Query Match 15.2%; Score 261.4; DB 8; Length 6048;
Best Local Similarity 51.8%; Pred. No. 8:9e-54;
Matches 743; Conservative 1; Mismatches 667; Indels 22; Gaps 6;

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QY 12 CAAGTTTGAGATGGACAAATATCAAAATGTTCAACAAAAGTCTGCTTT-GTAGTTATTG 70
DB 4390 CAATGTTAGAGGTGCAAAATATCATGCTTAGAACAACCACTGCGTTAATTTATTAG 4449

QY 71 ATGGATGGGGCCCTTCCGATGAACAACACGGGAATGCAATGTAAGATTAACACGCCCTA 130
DB 4450 ATGGTTTGGGAACCGGAAAGCAACATGTAATCGGTAAATATAGCAACAAGCCTA 4509

QY 131 TTATGACAAACCTTTGCTCGGAAT---TGGCAAAATTTGGAAGCACACGGTCTTCATG 187
DB 4510 ATTTGATCGTTTATCAACAATATCCACAGACTCAAAATCGAAGCGGTGGCTTAGATG 4569

QY 188 TTGGATTGCCAGAGGCTTAATGGGAATTTCTGAAGTTGGACATTTGAATATAGGAGCTG 247
DB 4570 TTGGACTACCTGAAGGACAAATGGTAACTCAGAAGTTGTCATATGAATATCGGTGACG 4629

QY 248 GAAGAGTATTATCAAGATATTGTTGCAATTAATTTGGCTGTTCAACGAAACAGATTTG 307
DB 4630 GACGTATCGTTTATCAAGTTTAACTCGAATCAATAATCAATTTGAAGACGGTGATTTCT 4689

QY 308 TTACAATCTCAGATTGTTGCATCAGCTGAGCGTCAAGAGAGGGAGTGGTCGATTGC 367
DB 4690 TTGAAATGATGTTTAAATATGCAATTCACACAGCTGAATTCACATGATTCAGCGTTAC 4749

QY 368 ATTTATTAGGACTGGTTAGCGATGGTGTCTCACTCTCATATTTGATCATCTTTTGGCGT 427
DB 4750 ACATCTTTGGTTTATGCTCGAGGTTGGTGTACACAGCTATTACAAACATTTATTGCTT 4809

QY 428 TGATAGCTGCATTAACAATTAACAAGTGCCAAAGGTTTTCATCTACTTTTTCGCTGATG 487
DB 4810 TGTTAGAACTTGCTTAAACAAACAGGTGTTGAAAAGTTTACGTACACGCAATTTTAGATG 4869

QY 488 GTCGAGATCTTCCCAACAAGTGGAGCTGTTATCTTGAAACATTTCTTCAATTTATTG 547
DB 4870 GCGGTGACGTAGTCAAAATCGCTTTGAAATACATCGNAGAGACTGAAGCTAAATTC 4929

QY 548 CTTTGGAAAGATACGGAGATTTGGCTTACTTACTGAGCTTATTATGCAATGGATFAGG 607
DB 4930 ATGAATTAGGCATTTGCTCAATTTGCTATCTGCTGCTGCTTATTATGCAATGGATCGTG 4989

QY 608 ACAAAAGATGGGACGCTATTAAGATCGCTTATGAGCAATTTGTTGAGGATTTGGACAA 667
DB 4990 ACAACGTTGGGAACGTGAAGAAAAGCTTACAATGCTATT-----CGTAATTTTGTG 5043

QY 668 AAGCCACCGTTGATAAGGTGTCGATGTTGTTAGAGGCGATATGCTCAATCTGAGACTG 727
DB 5044 CCCCACCTTATGCACTGCCAAGAAGAGGTGTAGAACAAGCTATATGAGGCGTTAACTG 5103

QY 728 ACGAATTTCTGAACCA---ATTGTTTTTTCGGACGATGGCGAGTAAAGATGACGATA 784
DB 5104 ACGAATTCGTAGTACCATTATCATCTTGAGAAATCAAAATACGGGTGTTAATGAGGAGATG 5163

QY 785 CTCTTATTTCTTCAATTTATCGTGTGATCGTATGCTGCTCAAAATTTGTAATGTTGGGTC 844
DB 5164 CAGTGAATCTTCAATTTATTTCCGACCTGTAGAGCAGCGCAATTTATCGGAATTTTTCGGA 5223

QY 845 TCGAAGCTTATAAAGATCTTAAATAGTTTCGTTCTCCCTCACCCCTAAAAATATTCAGAT 904
DB 5224 ACAGACCATTCGAGCGCTTAA-----AGTTGAACAAGTTAAGACTATTCTATGCA 5277

QY 905 GGATGACCAATACAAATAAGAGTTTCCATTTCCATCGTTATTTCCACCTGTGACTCAT 964
DB 5278 CATTCACATAAGTATATGACAATATCGATCGCGCTATCGCTCTTCGAAAAGTTGATTTAA 5337

QY 965 CTAATGCTGCTGTAATGGCTGCTTCTCAAGGAGTTACTCAATTTCTACTGTGCGGAA 1024
DB 965 CTAATGCTGCTGTAATGGCTGCTTCTCAAGGAGTTACTCAATTTCTACTGTGCGGAA 1024
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DB 5338 ATAATACAAATGGTGAATTTGCACAAAATAACAATTAACCTCAATTTACCTATTTCGAGAA 5397
QY 1025 CTGAGAAGTATCTCATGTTTACCTTCTCTTTAATGGTGTGCGAGAGTTCAATTTCAAG 1084
DB 5398 CTGAAAATAATACCTCAGTTTACTTATGAGTGGTGACCTAACGAGGAATTTAAAG 5457
QY 1085 ATGAAGAGGGTGTATGTTTCCCTCACAAAAGAAGTTGCTACATATGATTTAAAACCCAG 1144
DB 5458 GTCAACGCGTCTGTTTAAATTTGATTCACCTA---AAGTTGCAACGATGACTTCAACCCAG 5514
QY 1145 AATGATGCTGCTGGAGTTGCCGAAAATAATGTCGAGCAAAATGTCAGTCAGGACGATC 1204
DB 5515 AATGATGCTGCTGATGAAGTAAAGATGCAATTTATGAAGAGTTTAAATAAAGTGTGACTTGG 5574
QY 1205 CTTTGGCTTATGCAATTTTGGCCCTCTCACATGTTGACATCTGTCATACTGTAATTTCAAC 1264
DB 5575 ACTTAATTTTAAACTTTTGTAAACCTGATGTTGACATGTTGATGCTGCTTGAAGC 5634
QY 1265 CTGCCCTCAAGCATCTCAAGCTTACTGAGGAGGCAATTTGAAAAGATATTTGAAGCATGCC 1324
DB 5635 CGACAATCAAGCAATCGAAGCGTTGATGAATGTTTAGGAGAAGTGGTTGATAAGATTT 5694
QY 1325 AAATTTATTAATGCTTCTTATGTTTACTTCCGATCATGGAATGCTGAGAAGATGATTG 1384
DB 5695 TAGACATGAGCGGTTATGCAATTTATTTACTGCTGACCATGTAACCTCTGATCAAGTATGA 5754
QY 1385 CTCCCGATGCTAGTGAACATCTGACATACCTGCAATTTTGGTCCCATTTACT 1437
DB 5755 CGATGATGATCAACCAATGACTTACGCANACAGAACCCAGTACCAGTGATTT 5807
```

RESULT 2

US-09-895-913A-105
; Sequence 105, Application US/09895913A
; Patent No. US20020160456A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean Francois
; APPLICANT: Omen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160456A1 Helicobacter Polypeptides
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895, 913A
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 105
; LENGTH: 1620
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)....(1538)
US-09-895-913A-105

Query Match 12.9%; Score 222.2; DB 10; Length 1620;
Best Local Similarity 53.9%; Pred. No. 2e-44;
Matches 655; Conservative 0; Mismatches 518; Indels 42; Gaps 8;
QY 167 TGAAGCACACGCTCTTCATGTTGGATTGCCAGAGGCTTAATGGGAATTTCTGAAGTTG 226
DB 196 TTGATACGATGGCTTGGAGCTGTACCTTAAGGGGCAATGGGAATTTCTGAAGTTG 255
QY 227 GACATTTGAATATGAGGCTGGAAGAGTTTATTTATCAAGATATTTGTCGAATTTAAATTTGG 286
DB 256 GGCATATGTTATGGGCTGGTAGGCTCTCTATCAGGATTTAGTCAAAATTTCTTTAA 315
QY 287 CTGTTCAACGAAACGAGTTTGTTTACAAATCTCAGATTTGTCATCAGCTGAGCGTGCA 346

Db 648 GATGCGCTTGTCAAGAAATAGGCTGAAAGCATAAGCGCATCATCTCAACTTTGGC 707
QY 1228 CCTCTGACATGCTTGGACATCTACTATAATTGAACTTGCCTGCAAGCATCTCAAGCT 1287
Db 708 AACCTTGACATGCTTGGACATCTAGGAAAGTCGAGCCGCTCAAGCAATCGAAGCG 767
QY 1288 ACTGAGGAGCAATTTGAAAGATATTTAGAGCATGCAAACTTATAATTTACGTTCTTATG 1347
Db 768 GTTGACGAGTGTCTGCGCAAGTCGTTGATGCGATTCTTGCAAAAGCGCGCTACGGATT 827
QY 1348 GTTACTTCCGATCATGAAATGCTGAGAAGATGATTTGCTCCGATGCTAGTGAACATAT 1407
Db 828 ATTACGGCGACACGCTAACCGAGCTGCTGATTACCGAAGAGGCGAAGCGCACACC 887
QY 1408 GCACATACCTGCAATTTGGTCCCATTTA 1435
Db 888 GCACATACGACAAACCGGTTCTGTCA 915

RESULT 4

US-09-974-300-5220
; Sequence 5220, Application US/09974300
; Patent No. US2002014672A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: Expression
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5220
; LENGTH: 881
; TYPE: DNA
; ORGANISM: Bacillus clausii
US-09-974-300-5220

Query Match 9.4%; Score 161.2; DB 10; Length 881;
Best Local Similarity 52.7%; Pred. No. 1.5e-29;
Matches 436; Conservative 0; Mismatches 368; Indels 24; Gaps 3;
QY 561 CGGAGAAATGGCTACTATTACTGGAGCTTATTATGCAATGGATAGGACAAAGATGGGA 620
Db 50 CGGTAACTGGCGACTGTGCACGGCGTTACTATGCAATGGATCGGACAAACGTTGGGA 109
QY 621 GCGTATTAGATGGCTTATGAGGCAATTTGAGGATTTGACAAAGAACCCACCGTTGA 680
Db 110 TCGAGTTGAAAGTATACCTGCGCAATGTTTATGGCAGGCGC-----CTGCTATAA 163
QY 681 TAAGGCTGTCGATGTTGTAGAGAGATATGCTCAATCTGAGCTGACGAAATTTCTGAA 740
Db 164 GAACGGCTAGAGCTGTAGAGACAGCTTACAAAAACAACTTTGACGAGTTTGTCTAT 223
QY 741 ACCAATGCTTTTTCGGAGATGGCGA-----GTAAAGATGACGATAC 785
Db 224 TCCGCTGTATTACAGAGAGAAATGGTACACCTGTAGCACTGTCAAGACGATGACGC 283
QY 786 TCTTATTTTCTTCAATATPCTGCTGATGCTGCTCAAAATTTGTAATTTGGGTCT 845
Db 284 CGTCAATTTCTCAATTTTCGCCCTGACCGTCTATCAGCTATCAGATTCACAGTTTTCACGA 343
QY 846 CGAAGCTTATAAGATCTTAATAGTTCGTTCCCTCACCCATAAATATTCAGATTAGTG 905
Db 344 TGAAGACTTTCTGGGTTTCGACCGAGGGGAAAGATGCGAAACGCCCTCCATTTTGTCTG 403
QY 905 GATGCCCAATACATAAGAGTTTCCATTTCCATCGTTATTTCCACCTGTGACATCATAC 965

Db 404 CTTAAAGAAAGTTTACTGAAACAGTGAAGGCTTTTGTTCGCTTTAAGCGCACTAACTTGA 463
QY 966 TAATGCTGCTGCTGATGCTTCTTCAAGAGAGTTACTCAATTTCACTGTGCGCAAC 1025
Db 464 CAATACGCTTGGGAGTCTCTTTCCAGCAAGCTTACACAGCTACGAGTTGCGGAAC 523
QY 1026 TGAGAAGTATCTCATGTTTACCTTCTTTTAAATGCTGTCGAGAAGTTCAATTTCAAGA 1085
Db 524 CGAANAATACCCACATGTACGCTTCTTTTTCAGTGGCGGCTGAAGAAGAGTTTCCAGG 583
QY 1086 TGAAGAGCGTTTATGTTCCCTGACCAAAAGAGTTGCTACATATGATTTAAACCCAGA 1145
Db 584 CGAAGAGCGGATTTTATGATCGACTCGCTA---AAGTCGCTACTTACGACTTAAACCGGA 640
QY 1146 AATGAATGCTGCTGAGTTGCGGAAATAATGTCGAGCAAAATTTAGTCAGGAGGCGATCC 1205
Db 641 AATGAGCGCTTATGAAGTAACCGCTGCTCAAGGAATTCGAAGCGCAAAACATGA 700
QY 1206 TTTGTTATGTGCAATTTTGGCCCTCTGACATGTTGGACATCTACTGTTAAATTTGAACC 1265
Db 701 TGTGTTATCTTAACTTTTGCCCAACCTTGACATGTTGGGCACTCTGGAATGTTGAGCC 760
QY 1266 TGCCGCTCAAGCATGTCAAGCTACTGACGAGCAATTTGAAAGATATTTGAAGCATGCCA 1325
Db 761 AACAGTAAAGCGATTGAAGCGTTGACGAATGCTTAGGCCGTTGGTCTGATGCTTGT 820
QY 1326 AACTTATAATACGTTCTTATGTTTACTTCCGATCATGGAATGCTGA 1373
Db 821 TCAAAAGGCGGAGCGCGGATTTATTACAGCTACCAACGCAATGCGGA 868

RESULT 5

US-09-938-842A-2675
; Sequence 2675, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2675
; LENGTH: 1728
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2675

Query Match 4.9%; Score 84; DB 10; Length 1728;
Best Local Similarity 53.2%; Pred. No. 2.4e-10;
Matches 202; Conservative 0; Mismatches 175; Indels 3; Gaps 1;
QY 1006 CAATTTCTACTGTCGCGAACTGAGAAGTATCTCTATGTTACCTTCTCTTTAATGTTGT 1065
Db 1108 CATTTTCCCAATATGAGACCGTCAAGTTGGGATGTCACCTTCTCTGGAATGGAAT 1167
QY 1066 CGAGAAGTTCAATTTCCAAAGATGAAGAGCGTTGATGTTCCGTCACCAAAAGAGTTGCT 1125
Db 1168 CGATCTGATATTTCAACGAGAAATTTGGAGGAGTATGTTGAAATCCCAAGTCACAGTGA 1227
QY 1126 A---CATATGATTTAAACCAAGAAATGATCTGCTGAGTTGCGCGAATAATGTCGAG 1182
Db 1228 ATATCATTTCAATGTCACGCAAGATGAAGCTCTGGAAATTTGGTGAAGCAAGGAT 1287

Db 212 CCATTAT---TGAGGTATCACCGGATTTGGCATCAAGGTTTATTATACATGTAATCTAG 156
QY 485 ATGGTCGAGATCTTCGCCAACAAGTGGAGCTGTTATCTTGACAACTTCTCAATTTA 544
Db 155 ATGGTAGGAGTGT---CCACCGGTTCTGCTGAGAAATATATCGGTATGCTGAACGCTA 99
QY 545 TTCTTCGGAAGAGTAGTACGAGAAATTCGCTACTATTACTGACGCTTATTATGCAATGGATA 604
Db 98 AATTGAGCACITTAATGCGGAATTTGCTACTGTTGACGGCGTACTATGCTATGCTATGATA 39
QY 605 GGGACAAAGATGGGAGCGGTATTAAAGATGCTTATGA 641
Db 38 GGGATATCGCTCGGATAGGACATGTAAGAGCTTATGA 2

RESULT 8

US-08-781-986A-782
; Sequence 782, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 782:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-782

Query Match 4.0%; Score 69.4; DB 8; Length 400;
Best Local Similarity 49.9%; Pred. No. 4.3e-07;
Matches 195; Conservative 0; Mismatches 195; Indels 1; Gaps 1;
QY 233 TGAATATAGGAGCTGAAGAGTATTATCAAGATATTGTCGAATTAATTTGGCTGTTC 292
Db 2 TGAATATCGTGCAGGACGTATCGTTATCAAGTTTAACTCGATCAATAATCAATG 61
QY 293 ACAGAAAGAGTTTGTTCACAACTCCTCAGATGTTGTCATCAGCTGAGCGTGCAAAAGG 352
Db 62 AAGAGCGGTGATTTCTTTGAAATGATGTTTTAAATGCAATTCGACACGCTGAATTCAC 121
QY 353 GGAGTGGTGGATTTATGAGTATTATGAGTGGTTAGCGATGGTGGTCTCCACTCTCATATG 412
Db 122 ATGATTCAGCGTTACACATCTTTTGGTTTATTCTCTGACGGTGGTGTACAGCTCATTACA 181

QY 413 ATCATCTTTTTCGTTGATACGTGCAATTTAAACAATTTACAAGTGCCAAAGGTTTTCATTC 472
Db 182 ACATTTATTTTCTGTTTGTAGACACTTGTCTAAAACAAGNGTTGAAAAGTTTAGCTAC 241
QY 473 ACTTTTTCCTGATGGTCGAGATCTTCGCCAACAAGTGGAGCGTGTATCTTTGAACAAC 532
Db 242 ACGCATTTTATAGATGGCCGTGA-CGTAGATCAAAAATCCGCTTTGAAATACATCGAAGAG 300
QY 533 TTCCTCAATTTATTTGCTTCGGAAAAGTACGGAGAATTTGGCTACTATTACTGGACGTTATT 592
Db 301 ACTGAAGCTAAATCCATGAATNAGGCCATTTGCACGGGGCCTGGCCGTAATA 360
QY 593 ATGCAATGATAGGAGACAAAAGATGGGAGCG 623
Db 361 AGCCRAAGGACCGGCCAACCGTTGGGACCG 391

RESULT 9

US-09-974-300-894/c
; Sequence 894, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 894
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-894

Query Match 3.0%; Score 51.8; DB 10; Length 264;
Best Local Similarity 54.5%; Pred. No. 0.0074;
Matches 126; Conservative 0; Mismatches 102; Indels 3; Gaps 1;
QY 65 TTATTGATGGATGGGCGCTTTCCGATGAACACACGGGAATGCAATTTGCTAAAGCTAAAA 124
Db 261 TTTTAGATGGGTTTGGACTAAGGACGAAACCGTCGGAACCGCTAGCCCAAGCGAAAA 202
QY 125 CGCCTATTATGCAAAAACCTTTCTCTGGAATTTGG---CAAAAATTTGGAAGCACACGGTC 181
Db 201 AACCGAATTTGACCGCTATTGGACAAGTATCCGCACACAGAGCTGACAGGTTTCAGGAG 142
QY 182 TTCATGTTGGATTGCCAGAAGCTTTAATGGGAAATTTGAAAGTTGACATTTGAATATAG 241
Db 141 AAGCGGTAGTCTTCCAGAGCGCCAGATGGGCAACTCGGAAGCTCGGCCATCTGAATATCG 82
QY 242 GAGCTGGAAGAGTATTATTAAGATATTGTTGGAATTAATTTGGCTGTTC 292
Db 81 GCGCAGGCGGATCGTTTATCAAAAGTCTGACGCGGTGAACGTTGCGATTC 31

RESULT 10

US-09-294-093B-4299
; Sequence 4299, Application US/09294093B
; Patent No. US20010051395A1
; GENERAL INFORMATION:
; APPLICANT: Lalqudi, Raghunath, V.
; APPLICANT: Ito, Laura, Y
; APPLICANT: Sherman, Bradley, K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
; FILE REFERENCE: PL-0009 US

Query Match 2.3%; Score 39.8; DB 9; Length 2861;
Best Local Similarity 53.5%; Pred. No. 25;
Matches 83; Conservative 0; Mismatches 72; Indels 0

